

22910

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From: Mertz, Prema
Sent: Wednesday, August 16, 2000 9:07 AM
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Please search SEQ ID NO:16 with protein databases.

Thanks

Prema Mertz
Prema Mertz, Ph.D.

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U.S. Patent & Trademark Office

12

Edward Hart
Technical Info Specialist
STIC / Biotech
QMI 12C14 Tel: 305-9203

make hard
masonry of brick
dry stone
CMB 1991

PI Murakami K, Ueno N, Kato Y;
WPI: 91-075112/11.
DR N-PSDB; Q10891.

PT xenopus laevis bone morphogenetic protein and DNA encoding it -
PS Claim 2; Fig 3; 28p; English.
CC A Xenopus laevis liver-derived DNA library in Charon 28 vector, was
CC screened with a rat activin beta-A cDNA probe. Five clones were
CC isolated, including clone M3. They were subcloned in pUC19 and used
CC to transform competent E. coli. Transformation E. coli HB101/
CC pXAR3 coding for the M3 BMP was sequenced and the amino acid
CC sequence of M3 deduced from it.
See also Q10890 and Q10892-7.

SQ

Query Match 66.4%; Score 608; DB 1; Length 127;
Best Local Similarity 59.7%; Pred. No. 1.46e-53; Mismatches 21; Indels 0; Gaps 0;
Matches 71; Conservative 27; Bases 119 S 119

DB 9 HATKASINCDNSLUCCKDVKDIDGWWDWIKPEGYQINYCMGLCPMHIPGAGTG 68
1 RARRRTPTCEPATPLCRRDHYDQELGRWDWILQPEGYQINYCSCGCPHLAGSPGIA 60
QY 69 GSFHHTVNLNIKANNIQPAVNNSCCVPTKRRRLSMYFDRNNVVKTDIADMVEACCS 127
61 ASFHSAVFS-L-KANNPWPASTSCCVPTARRPLSLYLDHNGNYYKTDVPMVEACGS 119

RESULT 7

ID P60518 standard; Protein; 130 AA.
AC P60518;
DT 26-JUN-1991 (first entry)
DE Sequence of bovine inhibin B subunit.
KW Hormone; inhibin agonist; antagonist; reproductive; gonad.
OS Bos taurus.
FH Key
FT peptide 1:1.172
FT protein 17.3. .288
PN W08605076A.
PD 23-OCT-1986.
PF 14-APR-1986; AU00097.
PR 18-APR-1985; AU-000194.
PR 06-SEP-1985; AU-002320.
PR 29-OCT-1985; AU-003157.
PR 19-DEC-1985; AU-003960.
PR 01-JAN-1986; AU-059039.
PR 05-MAY-1986; CN-103459.
PR 02-APR-1987; AU-071015.
PA (BIOT-) BIOTECHN AUSTR PTY.
PA (MONTI) MONASH UNIV.
PA (HENR-) PRICE.
PA HENRY'S HOSPITAL.
PA (SVIN-) ST VINCENT'S INST MED RE.
PT Forage R, Stewart A, Robertson D, Dekretser DM;
DR WPI; 86-291547/44.
N-PSDB; N60427.

PT New polynucleotide sequences and recombinant DNA - encoding
PT inhibin and synthetic peptides useful for affecting gonadal
PT function.
PS Disclosure; Fig 6, 71p; English.
CC DNA encoding inhibin and inhibin or part, analogues, homologues or
CC precursors thereof when produced by recombinant techniques are also
CC claimed, as well as pharmaceutical compositions thereof. These may
CC be used as an inhibin agonist, antagonist or for eliciting an
CC antigenic response to affect gonadal function or reproductive
CC physiology.
SQ Sequence 288 AA:

Query Match 54.4%; Score 498; DB 1; Length 288;
Best Local Similarity 45.5%; Pred. No. 1.54e-41; Mismatches 32; Indels 2; Gaps 2;
Matches 55; Conservative 32; Bases 119 S 119

DB 10 RRRRGLECDGKVNICKKOFFVFSKFRDIDGWNDWIAFSGYHANYCGBECPSHIACTGSS 69
1 RARRRTPTCEPATPLCRRDHYDQELGRWDWILQPEGYQINYCSCGCPHLAGSPGIA 60
QY 168 RRRRGLECDGKVNICKKOFFVFSKFRDIDGWNDWIAFSGYHANYCGBECPSHIACTGSS 227
1 RARRRTPTCEPATPLCRRDHYDQELGRWDWILQPEGYQINYCSCGCPHLAGSPGIA 60
DB 228 LSFHSTVNLNIKANNIQPAVNNSCCVPTKRRRLSMYFDRNNVVKTDVPMVEACCS 287
QY 61 ASFHSAVFS-L-KANNPWPASTSCCVPTARRPLSLYLDHNGNYYKTDVPMVEACGS 119

DB 288 S 288
QY 119 S 119

RESULT 8

ID P60518 standard; Protein; 288 AA.
AC P60518;
DT 26-JUN-1991 (first entry)
DE Sequence of bovine inhibin B subunit.
KW Hormone; inhibin agonist; antagonist; reproductive; gonad.
OS Bos taurus.
FH Key
FT peptide 1:1.172
FT protein 17.3. .288
PN W08605076A.
PD 23-OCT-1986.
PF 14-APR-1986; AU00097.
PR 18-APR-1985; AU-000194.
PR 06-SEP-1985; AU-002320.
PR 29-OCT-1985; AU-003157.
PR 19-DEC-1985; AU-003960.
PR 01-JAN-1986; AU-059039.
PR 05-MAY-1986; CN-103459.
PR 02-APR-1987; AU-071015.
PA (BIOT-) BIOTECHN AUSTR PTY.
PA (MONTI) MONASH UNIV.
PA (HENR-) PRICE.
PA HENRY'S HOSPITAL.
PA (SVIN-) ST VINCENT'S INST MED RE.
PT Forage R, Stewart A, Robertson D, Dekretser DM;
DR WPI; 86-291547/44.
N-PSDB; N60427.

PT New polynucleotide sequences and recombinant DNA - encoding
PT inhibin and synthetic peptides useful for affecting gonadal
PT function.
PS Disclosure; Fig 6, 71p; English.
CC DNA encoding inhibin and inhibin or part, analogues, homologues or
CC precursors thereof when produced by recombinant techniques are also
CC claimed, as well as pharmaceutical compositions thereof. These may
CC be used as an inhibin agonist, antagonist or for eliciting an
CC antigenic response to affect gonadal function or reproductive
CC physiology.
SQ Sequence 288 AA:

Query Match 54.4%; Score 498; DB 1; Length 288;
Best Local Similarity 45.5%; Pred. No. 1.54e-41; Mismatches 32; Indels 2; Gaps 2;
Matches 55; Conservative 32; Bases 119 S 119

RESULT 9

ID P70203 standard; protein; 426 AA.

AC P70203; 09-APR-1991 (first entry)
 DT Sequence of human inhibin beta-chain precursor beta-A.
 DE Fertility control; contraception; hormone; spermatogenesis.
 KW Homo sapiens.
 OS Location/Qualifiers
 FT modified_site 155..167
 FT region 1..28
 FT /note="potential N-linked glycosylation sites"
 FT /note="signal sequence"
 FT 28..310
 FT /note="pro region"
 FT protein 311..326
 FT cleavage_site 306..310
 FT /note="proteolytic processing site"
 FT EP-222491-A.
 FT 20-MAY-1987.
 FT 02-OCT-1986; 307586.
 FT 03-OCT-1985; US-83910.
 PR 10-FEB-1986; US-827710.
 PR 12-SEP-1986; US-906729.
 PA (GETH) GENENTECH INC.
 PI Mason AJ, Seeburg PH.
 DR WPI; 87-137512/20.
 DR N-PSDB; N70315.
 PR Recombinant human or porcine inhibin or activin - used for modulating clinical condition or reproductive physiology of animals.
 PT Disclosure: Fig 8A: 48PP; English.
 CC A compsn. comprising human or porcine inhibin which is completely free of unidentified or porcine proteins is claimed. Also claimed are non chromosomal DNA encoding inhibin-alpha or an inhibin-beta chain. Sequencing of inhibin-encoding cDNA has led to the identification of prodomain regions located N-terminal to the mature inhibin chains that represent coordinately expressed biologically active polypeptides. The prodomain regions or prodomain immunogens are useful in monitoring preproinhibin processing in transformant cell culture or in experiments directed at modulating the clinical condit. or reproductive physiology of animals.
 CC Sequence 426 AA;

PT Physiologically active protein prepn. - by transforming plasmid having gene coding physiologically active protein and gene of dihydrofolic acid reductase to hamster ovary etc.
 PR Example 1; Fig 1; 12PP; Japanese.
 PS Gene may be expressed by transforming a dhfr negative strain of CHO cells with an active BUF-3 gene and dhfr carrying vector. BUF-3 gene product is a cell differentiating factor.
 CC Sequence 426 AA;

Query Match 54.4%; Score 498; DB 1; Length 426;
 Best Local Similarity 45.5%; Pred. No. 1.54e-41; Gaps 2;
 Matches 55; Conservative 32; Indels 2; Gaps 2;
 FT Protein 309..424
 FT Cleavage-site 304..308
 FT /note="proteolytic processing site"
 FT EP-222491-A.
 FT 20-MAY-1987.
 FT 02-OCT-1986; 307586.
 PR 03-OCT-1985; US-83910.
 PR 10-FEB-1986; US-827710.
 PR 12-SEP-1986; US-906729.
 PA (GETH) GENENTECH INC.
 PI Mason AJ, Seeburg PH.
 DR WPI; 87-137512/20.
 DR N-PSDB; N70315.
 PR Recombinant human or porcine inhibin or activin - used for modulating clinical condition or reproductive physiology of animals.
 PT Disclosure: Fig 2B: 48PP; English.
 CC A compsn. comprising human or porcine inhibin which is completely free of unidentified or porcine proteins is claimed. Also claimed are non chromosomal DNA encoding inhibin-alpha or an inhibin-beta chain. Sequencing of inhibin-encoding cDNA has led to the identification of prodomain regions located N-terminal to the mature inhibin chains that represent coordinately expressed biologically active polypeptides. The prodomain regions or prodomain immunogens are useful in monitoring preproinhibin processing in transformant cell culture or in experiments directed at modulating the clinical condit. or reproductive physiology of animals.
 CC Sequence 427 AA;

Query Match 54.4%; Score 498; DB 1; Length 427;
 Best Local Similarity 45.5%; Pred. No. 1.54e-41; Gaps 2;
 Matches 55; Conservative 32; Indels 2; Gaps 2;
 FT Protein 307..427
 FT Cleavage-site 304..427
 FT /note="proteolytic processing site"
 FT EP-222491-A.
 FT 20-MAY-1987.
 FT 02-OCT-1986; 307586.
 PR 03-OCT-1985; US-83910.
 PR 10-FEB-1986; US-827710.
 PR 12-SEP-1986; US-906729.
 PA (GETH) GENENTECH INC.
 PI Mason AJ, Seeburg PH.
 DR WPI; 90-055348/03.
 DR N-PSDB; Q01648.

AC P80019; (first entry)
 DT 28-JAN-1993
 DE Sequence of the 14K beta-chain of a protein exhibiting
 inhibin activity; inhibin; follicle stimulating hormone; inhibitor;
 KW fertility control; inhibin; gonadotropin.
 KW gonadotropin.
 OS Homo sapiens.
 PN US4737578A.
 PD 12-APR-1988.
 PF 07-APR-1986; 848924.
 PR 10-FEB-1986; US-828435.
 PR 07-APR-1986; US-848924.
 PA (SALK) SALK INST FOR BIOL STUD.
 PI Evans RM, Rosenfeld MG, Cerelli G, Mayo KE, Spiess J,
 Rivier JEF, Valenow;
 NPI: 88-119128-17.

New proteins with inhibin activity - esp. useful for controlling
 fertility in males

Claim 1: Column 7-8: 6pp; English.

The inventors claim 2 proteins - A and B - each of which has a
 molecular weight of about 32K and is comprised of an alpha (18K) and
 a beta (14K) chain of human inhibin. The alpha chain is P80018.
 The beta chain is either P80019 or P80020. Proteins A and B are
 useful for regulating fertility of mammals. Each 32K protein
 exhibits inhibin activity in basal secretion of FHS but not
 CC inhibiting basal secretion of luteinizing hormone (LH).

Sequence 116 AA;

Query Match 51.5%; Score 472; DB 1; Length 116;
 Best Local Similarity 45.1%; Pred. No. 1.02e-38; Matches 32; Gaps 2;
 Matches 51; Conservative 32; Mismatches 28; Indels 2;
 Db 4 CIGKVNICKKQFFVSKFDIGWMDNTIAPSGYHANYCFCGCTSHIAGTSGSSLRHSVTI 63
 Qy 9 CEPATPFCRQRHVDQELGWRDMLQEGYQDLYCSCGQCPPHAGSPGTAASPHSAVF 68
 Db 64 NHYRMQHSPPFANKSCCVPTKLROMSMYDDQONITKKDIONMIVEECCS 116
 Qy 69 S-L-LKANNPPASTSCCVPTARRPLSLVLDHNGNVVKTQPPDMVVEACGCS 119

Search completed: Thu Aug 17 10:15:45 2000
 Job time : 24 secs.



QY	61	ASPHSAVFSLLKANNPWPASTCCVPIRRPLSLYLIDHNGNVVKIDVPMV/VEACGCS	119
RESULT	2	S70580 #type complete	
ENTRY		activin beta C precursor - mouse	
TITLE		#formal_name Mus musculus #common_name house mouse	
ORGANISM		14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change	
DATE			
ACCESSIONS		S70580	
REFERENCE		570580	
#authors		Lau, A.L.; Nishimori, K.; Matzuk, M.M.	
#journal		Biochem. Biophys. Acta (1996) 1307:145-148	
#title		Structural analysis of the mouse activin beta-C gene.	
#cross-references		MUID:96288807	
#accession		S70580	
#status		preliminary	
#molecule-type		DNA	
#residues		1-352 #label LAU	
RIFCS		#cross-references EMBL:040772	
#introns		106/1	
CLASSIFICATION		#superfamily inhibin	
SUMMARY		#length 352 #molecular-weight 39401 #checksum 5176	
Query Match		Best Local Similarity 69.0%; Score 632; DB 2; Length 352;	
Matches		77; Conservative 26; Mismatches 16; Indels 2; Gaps 2;	
Db	232	RRRRGIDCGACASRMQCRQEFVDFREIGWUDWILQPEGYAMNFCGQCCPLHVAGMCGS 291	
QY	1	RARRRPTCPEPATPLCRRDHYDQGRWIDWILQPEGYOLNYCGQCPPLHAGSPGIA 60	
Db	292	ASFHATVLNLKANNIAGTGTGSSCCVPTSRRLPLSLYLIDHNGNVVKIDVPMV/VEACGCS 351	
QY	61	ASFHSAVFSLLKANNPWPASTCCVPIRRPLSLYLIDHNGNVVKIDVPMV/VEACGCS 118	
Db	352	S 352	
QY	119	S 119	
RESULT	3	JC3366 #type complete	
ENTRY		activin beta C - mouse	
TITLE		#formal_name Mus musculus #common_name house mouse	
ORGANISM		28-May-1997 #sequence_revision 18-Jul-1997 #text_change	
DATE		26-Aug-1999	
SESSIONS		JC3366	
REFERENCE		Fang, J.; Wang, S.; Smiley, E.; Bonadio, J.	
#authors		Biochem. Biophys. Res. Commun. (1997) 231:655-661	
#journal		Genes coding for mouse activin beta C and beta E are closely	
#title		linked and exhibit a liver-specific expression pattern in	
#cross-references		adult tissues.	
#accession		MUID:97224404	
#molecule-type		DNA	
#residues		1-352 #label FAN	
COMMENT		Activin beta C and beta E form a distinct subset of related	
GENETICS		activins.	
#introns		105/3	
CLASSIFICATION		#superfamily inhibin	
SUMMARY		#length 352 #molecular-weight 39387 #checksum 5265	
Query Match		Best Local Similarity 68.7%; Score 629; DB 2; Length 352;	
Matches		76; Conservative 27; Mismatches 16; Indels 2; Gaps 2;	
ACCESSIONS			
REFERENCE		JC2466	
#authors		Hoettgen, G.; Neidhardt, H.; Schneider, C.; Pohl, J.	
#journal		Biochem. Biophys. Res. Commun. (1995) 206:608-613	
#title		Cloning of a new member of the TGF-beta family: A putative	
#cross-references		MUID:95126961	
#accession		JC2466	
#molecule-type		mRNA	
#residues		1-352 #label HOE	
#cross-references		GB:X8250; NID:9669154; PIDN:CAA57890; 1; PID:9669155	

ENTRY 151199 #type complete
 TITLE activin beta B subunit - African clawed frog
 ORGANISM #formal_name Xenopus laevis #common_name African clawed frog
 16-Jul-1999
 151199
 151199
 ACCESSIONS
 REFERENCE #authors Dohrmann, C.E.; Hemmati-Brivanlou, A.; Thomsen, G.H.; Fields, A.; Woolf, T.M.; Melton, D.A.
 Dev. Biol. (1993) 157:474-483
 #title Expression of activin mRNA during early development in
 Xenopus laevis.
 #cross-references NID:93273083
 #accession 151199
 #status preliminary; translated from GB/EMBL/DBJ
 #molecule_type mRNA
 #residues 1-370 #label DOH
 #cross-references GB:S61773; NID:9386027; PIDN:AB26863.1; PID:9386028
 #length 370 #molecular_weight 41678 #checksum 6606
 #summary Local Similarity 51.7%; Score 474; DB 2; Length 370;
 #entry Match 48.3%; Pred. No. 5; DB 2; Length 370;
 #Matches 58; Conservative 25; Mismatches 36; Indels 1; Gaps 1;
 #residues 1-370 #label DOH
 Db 251 RIRRGLECDGRNLUCCRQFYIDFLRIGWNWIAPIGYGNCEGSCPAVLGVGSA 310
 Qy 1 RARRTPICEPATPLCCRRDHVDFQELGRWDWLQPEGLYOLNCSGOCPPHLAGSPGIA 60
 Db 311 SSFRTAVVNVQIRMGLNPGTVNNSCCIPKTLSSMSMLYFDEDEINVKRQPNMVEEGCA 370
 Qy 61 ASFHSAVFSILKANNPWPAST-SCCVPTARPLSLYLIDHNGNVVKTDVPMVWACGCS 119
 #classification #superfamily inhibin
 #accession NID:93273083
 #accession 13
 #entry JC4862 #type complete
 #status preliminary; translated from GB/EMBL/DBJ
 #molecule_type mRNA
 #residues 1-234 #label RES
 #organism Biochem. Biophys. Res. Commun. (1996) 224:451-456
 #date 15-Aug-1995 #sequence_revision 18-Oct-1996 #text_change
 16-Jul-1999
 #accession JC4862
 #authors Yamamoto, T.; Nakayama, Y.; Abe, S.
 #journal Biochem. Biophys. Res. Commun. (1996) 224:451-456
 #title Expression of activin beta subunit genes in seminiferous tubules of
 #newt testes.
 #cross-references NID:90295508
 #accession JC4862
 #molecule_type mRNA
 #residues 1-413 #label YAM
 #cross-references GB:D84516; NID:150288; PIDN:BAA12693.1;
 PID:91013374; PID:91502289
 #experimental_source testes
 #comment This protein is secreted from Sertoli cells and plays a role in the
 regulation of newt spermatogenesis.

CLASSIFICATION #superfamily inhibin
 FEATURE #domain signal sequence #status predicted #label SIG
 1-15 #product activin beta-A chain #status predicted #label
 #product activin beta-B chain #status predicted #label
 SUMMARY #length 413 #molecular_weight 4303 #checksum 5572
 #entry B41398 #type complete
 #title inhibin beta-B chain precursor - rat
 #alternate_names inhibin/activin beta B-chain
 #organism #formal_name Rattus norvegicus #common_name Norway rat
 16-Jul-1999
 153288; C40905
 #accession B41398
 #reference A41398
 #authors Feng, Z.M.; Li, Y.P.; Chen, C.L.C.
 Mol. Endocrinol. (1989) 3:1914-1925
 #journal Analyses of the 5'-flanking regions of rat inhibin alpha- and
 beta-B-subunit genes suggests two different regulatory
 mechanisms
 #cross-references NID:90190649
 #accession B41398
 #status preliminary
 #molecule_type DNA

ENTRY 14
 RESULT 14
 ENTRY 148235 #type fragment
 TITLE inhibin beta-B chain - mouse (fragment)
 ALTERNATE NAMES activin BB chain
 ORGANISM #formal_name Mus musculus #common_name house mouse
 02-Jul-1996 #sequence_revision 01-Aug-1997 #text_change
 16-Jul-1999
 148235; 148266; S31441
 #accession 148235
 #reference Ritvos, O.; Tuuri, T.; Ernster, M.; Sainio, K.; Hilden, K.;
 Saxon, L.; Gilbert, S.F.; Mech. Dev. (1995) 50:239-245
 #title Activin disrupts epithelial branching morphogenesis in
 developing glandular organs of the mouse.
 #cross-references NID:95344997
 #accession 148235
 #status preliminary; translated from GB/EMBL/DBJ
 #molecule_type mRNA
 #residues 1-234 #label RES
 #cross-references EMBL:83376; NID:9603571; PIDN:CAA58290.1;
 PID:903572
 #reference I48243
 #authors Albandi, R.M.; Groome, N.; Smith, J.C.
 #journal Development (1993) 117:711-723
 #title Activins are expressed in preimplantation mouse embryos and
 in ES and EC cells and are regulated on their
 differentiation.
 #cross-references NID:93221614
 #accession 148265
 #status preliminary; translated from GB/EMBL/DBJ
 #molecule_type mRNA
 #residues 134; D'136-225 #label ALB
 #cross-references EMBL:X69620; NID:960147; PIDN:CAA49326.1; PID:950148
 #classification #superfamily inhibin
 #summary #length 255 #checksum 6134
 #entry Match 51.4%; Score 471; DB 2; Length 255;
 #status preliminary; translated from GB/EMBL/DBJ
 #molecule_type mRNA
 #residues 1-234; D'136-225 #label ALB
 #cross-references EMBL:X69620; NID:960147; PIDN:CAA49326.1; PID:950148
 #accession 136 RIRRGLECDGRSLCRRQFFIDFLRIGWNWIAPIGYGNCEGSCPAVLGVGSA 195
 Qy 1 RARRTPICEPATPLCCRRDHVDFQELGRWDWLQPEGLYOLNCSGOCPPHLAGSPGIA 60
 Db 196 SSFRTAVVNVQIRMGLNPGTVNNSCCIPKTLSSMSMLYFDEDEINVKRQPNMVEEGCA 255
 Qy 61 ASFHSAVFSILKANNPWPAST-SCCVPTARPLSLYLIDHNGNVVKTDVPMVWACGCS 119
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 #entry B41398 #type complete
 #title inhibin beta-B chain precursor - rat
 #alternate_names inhibin/activin beta B-chain
 #organism #formal_name Rattus norvegicus #common_name Norway rat
 16-Jul-1999
 153288; C40905
 #accession B41398
 #reference A41398
 #authors Feng, Z.M.; Li, Y.P.; Chen, C.L.C.
 Mol. Endocrinol. (1989) 3:1914-1925
 #journal Analyses of the 5'-flanking regions of rat inhibin alpha- and
 beta-B-subunit genes suggests two different regulatory
 mechanisms
 #cross-references NID:90190649
 #accession B41398
 #status preliminary
 #molecule_type DNA

```

##residues 1-174 ##label FEN
##cross-references GB:M32755; GB:M32757; NID:9204943; PIDN:AAA41438.1;
REFERENCE
I33288
#authors Dykema, J.C.; Maio, K.E.
#journal Endocrinology (1994) 135:702-711
#title Two messenger ribonucleic acids encoding the common beta
B-chain of inhibin and activin have distinct 5'-initiation
sites and are differentially regulated in rat granulosa
cells.

#cross-references MUID:94:07180
I53288
#status Preliminary; translated from GB/EMBL/DDBJ
##molecule_type DNA
##residues 1-7 ##label RES
##cross-references GB:S72477; NID:9619268
REFERENCE
A44905
#authors Esch, F.S.; Shimasaki, S.; Cooksey, K.; Mercado, M.; Mason,
A.J.; Ying, S.Y.; Ueno, N.; Ling, N.
#journal Mol. Endocrinol. (1987) 1:388-396
#title Complementary deoxyribonucleic acid (cDNA) cloning and DNA
sequence analysis of rat ovarian inhibins.

#cross-references MUID:90331931
#accession C40905
#status Preliminary; not compared with conceptual translation
##molecule_type mRNA
##residues 133-411 ##label ESC
CLASSIFICATION #superfamily inhibin
SUMMARY #length 411 #molecular-weight 45182 #checksum 2167

Query Match 51.4%; Score 471; DB 2; Length 411;
Best Local Similarity 48.3%; Pred. No. 2, 98-88;
Matches 58; Conservative 27; Mismatches 34; Indels 1; Gaps 1;

DB 292 RIRKRKLECGRTSICRCQOFFIFRFLIGWNWDIAPIPGYYGMYCEESCPAYLAGVGSA 351
QY 1 RARRRIPTCBPAFLCRRDHIVPQELGRWDRMILQPEGIQLNICSQGCPPLAGSPGIA 60
DB 352 SSFHTAVVNGYRMGGLNPGVNSCRIPTLSSMMLYDDEYVNVKRPVNPMLVSCGCA 411
QY 61 ASFHSAAVFSLLKANNPWPAST-SCCVPTARRPLSLYLDHNGNVKTDVPMWVACGCS 119

Search completed: Thu Aug 17 10:16:42 2000
Job time : 39 secs.

```


CC LENGTH: 119 amino acids
 CC TYPE: amino acids
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: protein
 CC HYPOTHETICAL: NO
 CC ANTI-SENSE: NO
 CC FRAGMENT TYPE: internal
 CC ORIGINAL SOURCE: CN;
 SQ SEQUENCE 119 AA; 13161 MW; 75307 CN;
 Query Match Similarity 100.0%; Score 916; DB 8; Length 119;
 Best Local Similarity 100.0%; Pred. No. 4 26e-104; Length 119;
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 RARRRTPTCEPATPLCRRDRHVDFOELGRWDWILQPEGYQOLNYCSGQCOPPHLAGSPGIA 60
 Qy 1 RARRRTPTCEPATPLCRRDRHVDFOELGRWDWILQPEGYQOLNYCSGQCOPPHLAGSPGIA 60
 Db 61 ASFHSAVFSILKANNPWPASTSCCVPTARRPLSLYLDHNGNVVTKTDVPMVVACGCS 119
 Qy 61 ASFHSAVFSILKANNPWPASTSCCVPTARRPLSLYLDHNGNVVTKTDVPMVVACGCS 119

RESULT 2 ID US-09-184-933-12 STANDARD; PRT; 119 AA.
 ID US-09-184-933-12 STANDARD; PRT; 119 AA.
 XX DE Sequence 12, Application US/09184933
 CC Sequence 12, Application US/09184933
 CC Sequence 12, Application US/09184933
 CC GENERAL INFORMATION:
 CC APPLICANT: Lee, Se-Jin
 CC APPLICANT: Esqueala, Aurora F.
 CC NUMBER OF SEQUENCES: 12
 CC CORRESPONDENCE ADDRESS:
 CC APPLICANT: Lee, Se-Jin
 CC ADDRESS: Fish & Richardson, P.C.
 CC STREET: 4225 Executive Square, Suite 1400
 CC CITY: La Jolla
 CC STATE: CA
 CC ZIP: 92037
 CC COMPUTER READABLE FORM:
 CC COMPUTER: IBM Compatible
 CC OPERATING SYSTEM: Windows95
 CC SOFTWARE: FastSEQ for Windows Version 2.0
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/09/184, 933
 CC FILING DATE: 08/27/1999
 CC CLASSIFICATION: 536
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Haile, P.R.D., Lisa A.
 CC REGISTRATION NUMBER: 38, 347
 CC REFERENCE/DOCKET NUMBER: 07265/040001
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 212/7765-5070
 CC TELEFAX: 212/258-2281
 CC INFORMATION FOR SEQ ID NO: 12:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 119 amino acids
 CC TYPE: amino acid
 CC STRANDEDNESS: not relevant
 CC TOPOLOGY: both
 CC MOLECULE TYPE: protein
 SQ SEQUENCE 119 AA; 13161 MW; 75307 CN;
 Query Match Similarity 100.0%; Score 916; DB 7; Length 119;
 Best Local Similarity 100.0%; Pred. No. 4 26e-104; Length 119;
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 RARRRTPTCEPATPLCRRDRHVDFOELGRWDWILQPEGYQOLNYCSGQCOPPHLAGSPGIA 60
 Qy 1 RARRRTPTCEPATPLCRRDRHVDFOELGRWDWILQPEGYQOLNYCSGQCOPPHLAGSPGIA 60
 Db 61 ASFHSAVFSILKANNPWPASTSCCVPTARRPLSLYLDHNGNVVTKTDVPMVVACGCS 119
 Qy 61 ASFHSAVFSILKANNPWPASTSCCVPTARRPLSLYLDHNGNVVTKTDVPMVVACGCS 119

RESULT 4 ID US-60186-656-992 STANDARD; PRT; 131 AA.
 XX AC XXXXX
 XX DT
 DE Sequence 992, Application US/60186656
 CC GENERAL INFORMATION:
 CC APPLICANT: Bonazzi, Vivien
 CC TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS, AND
 CC TITLE OF INVENTION: NUCLEAR ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
 CC TITLE OF INVENTION: USES THEREOF
 FILE REFERENCE: CL000320
 CURRENT APPLICATION NUMBER: US/60/186,656
 CURRENT FILING DATE: 2000-03-03
 NUMBER OF SEQ ID NOS: 1318
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 992
 LENGTH: 131
 TYPE: PRT
 ORGANISM: HUMAN
 SQ SEQUENCE 131 AA; 14330 MW; 90159 CN;
 Query Match 100.0%; Score 916; DB 3; Length 131;
 Best Local Similarity 100.0%; Pred. No. 4.26e-104;
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 13 RARRTPCEPATPLCRRDHVDFQELGWRDWTIOPEGYOLNYCSCGCPPLAGSPGIA 72
 QY 1 RARRTPCEPATPLCRRDHVDFQELGWRDWTIOPEGYOLNYCSCGCPPLAGSPGIA 60
 Db 73 ASFHSAVSLKANNPWPASTSCCVPTARPLSLYLDHNGNVKTDVPMVACGCS 131
 Qy 61 ASFHSAVSLKANNPWPASTSCCVPTARPLSLYLDHNGNVKTDVPMVACGCS 119
 RESULT 5 ID US-60-185-361-608 STANDARD; PRT; 153 AA.
 XX AC XXXXX
 XX DT
 DE Sequence 608, Application US/60185361
 CC GENERAL INFORMATION:
 CC APPLICANT: Bonazzi, Vivien
 CC TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS, AND
 CC TITLE OF INVENTION: NUCLEAR ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
 CC TITLE OF INVENTION: USES THEREOF
 FILE REFERENCE: CL000291
 CURRENT APPLICATION NUMBER: US/60/185,361
 CURRENT FILING DATE: 2000-02-28
 NUMBER OF SEQ ID NOS: 968
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 608
 LENGTH: 153
 TYPE: PRT
 ORGANISM: HUMAN
 SQ SEQUENCE 153 AA; 16813 MW; 120970 CN;
 Query Match 100.0%; Score 916; DB 3; Length 153;
 Best Local Similarity 100.0%; Pred. No. 4.26e-104;
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 95 ASFHSAVSLKANNPWPASTSCCVPTARPLSLYLDHNGNVKTDVPMVACGCS 153
 QY 61 ASFHSAVSLKANNPWPASTSCCVPTARPLSLYLDHNGNVKTDVPMVACGCS 119
 RESULT 6 ID US-60-212-356-257 STANDARD; PRT; 274 AA.
 XX AC XXXXX
 XX DT
 DE Sequence 257, Application US/60212356
 CC GENERAL INFORMATION:
 CC APPLICANT: Brasley, Ellen
 CC TITLE OF INVENTION: ISOLATED HUMAN PHOSPHOLIPASE PROTEINS, AND
 CC TITLE OF INVENTION: NUCLEAR ACID MOLECULES ENCODING HUMAN PHOSPHOLIPASE
 CC TITLE OF INVENTION: PROTEINS, AND USES THEREOF
 FILE REFERENCE: CL000577
 CURRENT APPLICATION NUMBER: US/60/212,356
 CURRENT FILING DATE: 2000-06-19
 NUMBER OF SEQ ID NOS: 411
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 257
 LENGTH: 274
 TYPE: PRT
 ORGANISM: HUMAN
 SQ SEQUENCE 274 AA; 29976 MW; 36976 CN;
 Query Match 100.0%; Score 916; DB 23; Length 274;
 Best Local Similarity 100.0%; Pred. No. 4.26e-104;
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 156 RARRTPCEPATPLCRRDHVDFQELGWRDWTIOPEGYOLNYCSCGCPPLAGSPGIA 215
 QY 1 RARRTPCEPATPLCRRDHVDFQELGWRDWTIOPEGYOLNYCSCGCPPLAGSPGIA 60
 Db 216 ASFHSAVSLKANNPWPASTSCCVPTARPLSLYLDHNGNVKTDVPMVACGCS 274
 Qy 61 ASFHSAVSLKANNPWPASTSCCVPTARPLSLYLDHNGNVKTDVPMVACGCS 119
 RESULT 7 ID US-09-521-978-4 STANDARD; PRT; 350 AA.
 XX AC XXXXX
 XX DT
 DE Sequence 4, Application US/09521978
 CC Sequence 4, Application US/09521978
 CC GENERAL INFORMATION:
 CC APPLICANT: Ford, John E.
 CC APPLICANT: Mike, Nancy K.
 CC APPLICANT: Dickson, Mark C.
 CC APPLICANT: Arterburn, Matthew C.
 CC TITLE OF INVENTION: Methods And Materials Relating To Novel
 CC TITLE OF INVENTION: Activin/Inhibin-Like Polypeptides
 CC FILE REFERENCE: HYC-2
 CC CURRENT APPLICATION NUMBER: US/09/521,978
 CURRENT FILING DATE: 2000-03-09
 NUMBER OF SEQ ID NOS: 4
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 4
 LENGTH: 350
 TYPE: PRT
 ORGANISM: Homo sapiens
 SQ SEQUENCE 350 AA; 38561 MW; 616706 CN;

Query Match 100.0%; Score 916; DB 21; Length 350;
 Best Local Similarity 100.0%; Pred. No. 4.26e-104; No. Mismatches 0; Indels 0; Gaps 0;
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 232 RARRRTPTCEPATPLCRRDHVDFQELGWRDILQPEGYQLNCSGQCPPLLAGSPGIA 291
 QY 1 RARRRTPTCEPATPLCRRDHVDFQELGWRDILQPEGYQLNCSGQCPPLLAGSPGIA 60

Db 292 ASFHSAVSLKANNPWPASTSCCVTPARRPLSILYLDINGNVKTDVPMVACGCS 350
 QY 61 ASFHSAVSLKANNPWPASTSCCVTPARRPLSILYLDINGNVKTDVPMVACGCS 119

RESULT 8 ID US-08-311-370A-14 STANDARD; PRT; 350 AA.
 DE XX
 AC XXXXXX
 DT XX
 Sequence 14, Application US/08311370A
 GENERAL INFORMATION:
 APPLICANT: LEE, SE-JIN
 APPLICANT: ESKQUELA, AURORA F.
 TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-12
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Spansley Horn Jubas & Lubitz
 CITY: Los Angeles
 STATE: CA
 COUNTY: USA
 ZIP: 90067

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASSEQ Version 1.5

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/311,370A
 FILING DATE: 26-SEP-1994
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/274,215
 FILING DATE: 13-JUL-1994

ATTORNEY/AGENT INFORMATION:
 NAME: Halle, Ph.D., Lisa A.
 REGISTRATION NUMBER: 38,347
 ATTORNEY/DOCKET NUMBER: PD-3830

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619-455-5100
 TELEFAX: 619-455-5110
 TELEX: 619-455-5110

INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 350 amino acids
 TYPE: amino acids
 STRANDEDNESS: single

TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: internal
 ORIGINAL SOURCE:
 SEQUENCE 350 AA; 38561 MW; 616706 CN;

TELEX:
 IN INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 350 amino acids
 TYPE: amino acids
 STRANDEDNESS: single

TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: internal
 ORIGINAL SOURCE:
 SEQUENCE 350 AA; 38561 MW; 616706 CN;

Query Match 99.7%; Score 913; DB 13; Length 350;
 Best Local Similarity 99.2%; Pred. No. 1.07e-103; No. Mismatches 1; Indels 0; Gaps 0;
 Matches 118; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 232 RARRRTPTCEPATPLCRRDHVDFQELGWRDILQPEGYQLNCSGQCPPLLAGSPGIA 291
 QY 1 RARRRTPTCEPATPLCRRDHVDFQELGWRDILQPEGYQLNCSGQCPPLLAGSPGIA 60

Db 292 ASFHSAVSLKANNPWPASTSCCVTPARRPLSILYLDINGNVKTDVPMVACGCS 350
 QY 61 ASFHSAVSLKANNPWPASTSCCVTPARRPLSILYLDINGNVKTDVPMVACGCS 119

RESULT 9 ID US-08-752-919-6 STANDARD; PRT; 350 AA.
 DE XX
 AC XXXXXX

Sequence 6, Application US/08752919
 GENERAL INFORMATION:
 APPLICANT: Bonadio, Jeffrey
 TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES
 NUMBER OF SEQUENCES: 72
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Penile & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: NY
 COUNTRY: USA
 ZIP: 10036/711

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastaSQ Version 2.0

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/752,919
 FILING DATE: 20-NOV-1996
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Goruzzi, Laura A.
 REGISTRATION NUMBER: 30,742
 REFERENCE/DOCKET NUMBER: 8464-015
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-790-9090
 TELEFAX: 212-869-8864
 TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 350 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE 350 AA; 38517 MW; 615058 CN;

Query Match 99.7%; Score 913; DB 13; Length 350;
 Best Local Similarity 99.2%; Pred. No. 1.07e-103; No. Mismatches 1; Indels 0; Gaps 0;
 Matches 118; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 232 RARRRTPTCEPATPLCRRDHVDFQELGWRDILQPEGYQLNCSGQCPPLLAGSPGIA 291
 QY 1 RARRRTPTCEPATPLCRRDHVDFQELGWRDILQPEGYQLNCSGQCPPLLAGSPGIA 60

Db 292 ASFHSAVSLKANNPWPASTSCCVTPARRPLSILYLDINGNVKTDVPMVACGCS 350
 QY 61 ASFHSAVSLKANNPWPASTSCCVTPARRPLSILYLDINGNVKTDVPMVACGCS 119

RESULT 10 ID US-08-752-919-13 STANDARD; PRT; 251 AA.
 DE XX
 AC XXXXXX

Query Match 88.0%; Score 806; DB 3; Length 104;
 Best Local Similarity 100.0%; Pred. No. 1. 96e-89; 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 104; Conservative

Db 1 CORRRHYDFOELGRDWLQPEGGYQNYCSCQCPPLAGSPGIAASFHSAVFLKKA 73
 Qy 16 CORRRHYDFOELGRDWLQPEGGYQNYCSCQCPPLAGSPGIAASFHSAVFLKANN 75

RESULT 13 ID US-60-169-840-7660 STANDARD; PRT; 112 AA.
 XX AC XXXXXX DT

Sequence 7660, Application US/60169840
 GENERAL INFORMATION:
 APPLICANT: Bonazzi, Vivien
 TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS
 TITLE OF INVENTION: NUCLEAR ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS AND
 TITLE OF INVENTION: USES THEREOF
 FILE REFERENCE: CL000164
 CURRENT FILING DATE: 1998-12-09
 NUMBER OF SEQ ID NOS: 9128
 SEQ ID NO 7660
 LENGTH: 112
 TYPE: PRT
 ORGANISM: Human
 SQ SEQUENCE 112 AA; 12324 MW; 66422 CN;

Query Match 89.3%; Score 818; DB 3; Length 112;
 Best Local Similarity 100.0%; Pred. No. 4. 97e-91; 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 105; Conservative

Db 8 PLCCRRHYDFOELGRDWLQPEGGYQNYCSCQCPPLAGSPGIAASFHSAVFLKKA 67
 Qy 14 PLCCRRDHVDFQELGRDWLQPEGGYQNYCSCQCPPLAGSPGIAASFHSAVFLKKA 73

Db 68 NNPWPASTSCCVPTARRPLSLYLIDHNGNVVKTDVPMVVEACGC 112
 Qy 74 NNPWPASTSCCVPTARRPLSLYLIDHNGNVVKTDVPMVVEACGC 118

RESULT 14 ID US-60-163-123-1750 STANDARD; PRT; 104 AA.
 XX DT XXXXXX

Sequence 1750, Application US/60163123
 GENERAL INFORMATION:
 APPLICANT: Bonazzi, Vivien
 TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS
 TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS AND
 TITLE OF INVENTION: USES THEREOF
 FILE REFERENCE: CL000137
 CURRENT FILING DATE: 1999-11-02
 NUMBER OF SEQ ID NOS: 1986
 SEQ ID NO 1750
 LENGTH: 104
 TYPE: PRT
 ORGANISM: Human
 SQ SEQUENCE 104 AA; 11454 MW; 58103 CN;

Query Match 88.0%; Score 806; DB 3; Length 104;
 Best Local Similarity 100.0%; Pred. No. 2. 10e-66; 2; Mismatches 2; Indels 2; Gaps 2;
 Matches 77; Conservative

Db 232 RVRRGIDQGASRMCCRQEFDVFRIGWIDWILQPEGGYAMNFGTGOCPHLVAGMPGTS 291
 Qy 1 RAIRTPCPEPATPLCRRDHVDFQELGRDWLQPEGGYQNYCSCQCPPLAGSPGIAASFHSAVFLKANN 60

Query Match 69.0%; Score 632; DB 13; Length 352;
 Best Local Similarity 63.6%; Pred. No. 2. 10e-66; 2; Mismatches 16; Indels 2; Gaps 2;
 Matches 77; Conservative

Db 292 ASFHTAVILKANAAAGTGTGSCCVPTARRPLSLYLIDHNGNVVKTDVPMVVEACGC 351
 Qy 61 ASFISAVFSLKANNP-PAS-TSCCVPTARRPLSLYLIDHNGNVVKTDVPMVVEACGC 118

Db 352 S 352

Thu Aug 17 10:22:12 2000

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Page 7

QY 119 S 119

Search completed: Thu Aug 17 10:23:58 2000
Job time : 191 secs.

CC FRAGMENT TYPE: internal
 CC ORIGINAL SOURCE: CN;
 SQ SEQUENCE 119 AA; 13161 MW; 75307 CN;
 Query Match 100.0%; Score 916; DB 4; Length 119;
 Best Local Similarity 100.0%; Pred. No. 2.84e-81; Indels 0; Gaps 0;
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 RARRTPCEPATPLCCRRDHYDFQELGRDWLWQPGYQLNCSGOCPPHLAGSPGIA 60
 QY 1 RARRTPCEPATPLCCRRDHYDFQELGRDWLWQPGYQLNCSGOCPPHLAGSPGIA 60
 Db 61 ASHSAVFSLLKANNPWPASTSCCPTTARPLSLYLDDHNGNTVKTDVPMVVERGCS 119
 QY 61 ASHSAVFSLLKANNPWPASTSCCPTTARPLSLYLDDHNGNTVKTDVPMVVERGCS 119
 61 ASHSAVFSLLKANNPWPASTSCCPTTARPLSLYLDDHNGNTVKTDVPMVVERGCS 119
 61 ASHSAVFSLLKANNPWPASTSCCPTTARPLSLYLDDHNGNTVKTDVPMVVERGCS 119
 RESULT 2 ID US-08-765-662-12 STANDARD; PRT: 119 AA.
 XX AC xxxxxx
 DE Sequence 12, Application US/08765662
 CC Sequence 12, Application US/08765662
 CC Patent No. 5939213
 CC GENERAL INFORMATION:
 APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
 TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-12
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson
 STREET: 4225 Executive Square, Suite 1400
 CITY: La Jolla
 STATE: CA
 ZIP: 92037
 COUNTRY: USA
 CC COMPUTER READABLE FORM:
 CC COMPUTER: IBM Compatible
 CC COMPUTER TYPE: Diskette
 CC OPERATING SYSTEM: DOS
 CC SOFTWARE: FASTSEQ Version 1.5
 CC CURRENT APPLICATION DATA:
 CC COMPUTER READABLE FORM:
 CC COMPUTER: IBM Compatible
 CC COMPUTER TYPE: Diskette
 CC OPERATING SYSTEM: Windows95
 CC SOFTWARE: FASTSEQ for Windows Version 2.0
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/765,662
 CC FILING DATE: 28-APR-1997
 CC CLASSIFICATION: 536
 CC PRIORITY APPLICATION NUMBER:
 CC FILING DATE:
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Hale, Ph.D., Lisa A.
 CC REGISTRATION NUMBER: 38,347
 CC REFERENCE/DOCKET NUMBER: 07265/042W01 (FD-3930)
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 619-678-5070
 CC TELEFAX: 619-678-5099
 CC INFORMATION FOR SEQ ID NO: 12:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 119 amino acids
 CC TYPE: amino acid
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: protein
 CC FRAGMENT TYPE: internal
 SQ SEQUENCE 119 AA; 13161 MW; 75307 CN;
 Query Match 100.0%; Score 916; DB 2; Length 119;
 Best Local Similarity 100.0%; Pred. No. 2.84e-81; Indels 0; Gaps 0;
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 RARRTPCEPATPLCCRRDHYDFQELGRDWLWQPGYQLNCSGOCPPHLAGSPGIA 60
 QY 1 RARRTPCEPATPLCCRRDHYDFQELGRDWLWQPGYQLNCSGOCPPHLAGSPGIA 60
 Db 61 ASHSAVFSLLKANNPWPASTSCCPTTARPLSLYLDDHNGNTVKTDVPMVVERGCS 119
 QY 61 ASHSAVFSLLKANNPWPASTSCCPTTARPLSLYLDDHNGNTVKTDVPMVVERGCS 119

QY 61 ASFHSAVFLKANNPWPASTSCCVPTARRPLSLYLHDHGNVVKTDVPMVVEAGCS 119
 RESULT 4
 ID PCT-US95-08745-14 STANDARD; PRT; 350 AA.
 XX XX
 AC XXXXX
 XX DT
 XX DE Sequence 14, Application PC/TUS9508745
 XX Sequence 14, Application PC/TUS9508745
 CC GENERAL INFORMATION:
 CC APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
 CC TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-12
 CC NUMBER OF SEQUENCES: 14
 CC CORRESPONDENCE ADDRESS:
 CC APPLICANT: Fish & Richardson
 CC ADDRESS: 4225 Executive Square, Suite 1400
 CC CITY: La Jolla
 CC STATE: CA
 CC ZIP: 92037
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Diskette
 CC COMPUTER: IBM Compatible
 CC OPERATING SYSTEM: DOS
 CC SOFTWARE: FASTSEQ Version 1.5
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: PCT/US95/08745
 CC FILING DATE: 12-JUL-1995
 CC CLASSIFICATION:
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Haile, Ph.D., Lisa A
 CC REGISTRATION NUMBER: 38,347
 CC REFERENCE/DOCKET NUMBER: 07265/042W01 (FD-3830)
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 619-678-5099
 CC TELEX:
 CC INFORMATION FOR SEQ ID NO: 14:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 350 amino acids
 CC TYPE: amino acids
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: protein
 CC HYPOTHETICAL: NO
 CC ANTI-SENSE: NO
 CC FRAGMENT TYPE: internal
 CC ORIGINAL SOURCE:
 CC SEQUENCE 350 AA: 38561 MW: 616706 CN:
 Query Match 100.0%; Score 916; DB 4; Length 350;
 Best Local Similarity 100.0%; Pred. No. 2,84e-81; Gaps 0;
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC ORIGINAL SOURCE:
 CC SEQUENCE 350 AA: 38561 MW: 616706 CN:
 Query Match 100.0%; Score 916; DB 2; Length 350;
 Best Local Similarity 100.0%; Pred. No. 2,84e-81; Gaps 0;
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 232 RARRRTPTCEPATPLCCRDRHYDVFQELGWRWILQPEGYQLNCSGQCPHLAGSPGIA 291
 QY 1 RARRRTPTCEPATPLCCRDRHYDVFQELGWRWILQPEGYQLNCSGQCPHLAGSPGIA 60
 QY 1 RARRRTPTCEPATPLCCRDRHYDVFQELGWRWILQPEGYQLNCSGQCPHLAGSPGIA 60
 DB 292 ASFHSAVFLKANNPWPASTSCCVPTARRPLSLYLHDHGNVVKTDVPMVVEAGCS 350
 QY 61 ASFHSAVFLKANNPWPASTSCCVPTARRPLSLYLHDHGNVVKTDVPMVVEAGCS 119
 RESULT 5
 ID US-08-765-662-14 STANDARD; PRT; 350 AA.
 XX Sequence 4, Application US/08482577B
 AC Sequence 4, Application US/08482577B
 XX Patent No. 5807113
 DT

GENERAL INFORMATION:

CC APPLICANT: HOTTEN, GERTRUD
CC APPLICANT: NEIDHARDT, HELENE
CC APPLICANT: BECHHOLD, ROLF
CC APPLICANT: FOHL, JENS
CC TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL
CC TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS
CC NUMBER OF SEQUENCES: 49
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: NIKARDO, MARMELSTEIN, MURRAY, AND ORAM
CC STREET: 655 FIFTEENTH STREET, N.W., G STREET LOBBY,
CC SUITE 330
CC CITY: WASHINGTON
CC STATE: DC
CC COUNTRY: USA
CC ZIP: 20005
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-POS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.3.0
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/482,577B
CC FILING DATE:
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: KLEISNER, SHARON
CC REGISTRATION NUMBER: 36,335
CC REFERENCE/DOCKET NUMBER: P564-5-010
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202/638-5000
CC TELEFAX: 202/638-4810
CC INFORMATION FOR SEQ ID NO: 4:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 352 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC MOLECULE TYPE: Peptide
CC PUBLICATION INFORMATION:
CC DOCUMENT NUMBER: US 08/289,222
CC FILING DATE: 12-AUG-1994
CC SEQUENCE 352 AA; 39387 MW; 619423 CN;

Query Match 68-78: Score 629; DB 1; Length 352; Best Local Similarity 62.8%; Pred. No. 6.57e-52; Matches 76; Conservative 27; Mismatches 16; Indels 2; Gaps 2;

Db 232 RYRRRGIDCGGSRMCCRCRPFVPRFGNDWIDPQEGYAMNCMGCGOPLHVAGMFGIS 291
1 RARRRPCTCEPATPLCRRDHYDQELGWRDMLQPEGYOLNCGOCPPPHLGSFGIA 60

Db 292 ASPHATVNLKANNAAAGTGGGCCVTSRRLSLYDSDNTVKTDPDMVYAGC 351
Qy 61 ASFSAVESLILKANNPWPAS-TISCCVTPARPLSLYLDRANGNVVKTDPDMVYAGC 118

Db 352 S 352
Qy 119 S 119

RESULT 7 ID US-08-455-550-11 STANDARD: PRT; 127 AA.

DE Sequence 11, Application US/08455550
XX Sequence 11, Application US/08455550
CC Patent No. 567338
CC GENERAL INFORMATION:

CC APPLICANT: MURAKAMI, KAZUO
CC APPLICANT: UENO, NAOTO
CC APPLICANT: KATO, YUKIO
CC TITLE OF INVENTION: XENOPUS LAEVIS BONE MORPHOGENETIC PROTEINS AND USE THE
CC NUMBER OF SEQUENCES: 22
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Dike, Bronstein, Roberts & Cushman
CC STREET: 130 Water Street
CC CITY: Boston
CC STATE: MA
CC COUNTRY: USA
CC ZIP: 02109
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Disquette
CC COMPUTER: IBM Compatible
CC OPERATING SYSTEM: DOS
CC SOFTWARE: FASTSEQ Version 1.5
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/455,550
CC FILING DATE: 31-MAY-1995
CC CLASSIFICATION: 514
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/056,564
CC FILING DATE: 30-APR-1993
CC APPLICATION NUMBER: 07/577,892
CC FILING DATE: 05-SEP-1990
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Eisenstein, Ronald I
CC REGISTRATION NUMBER: 30628
CC REFERENCE/DOCKET NUMBER: 40302-FMC-DIV
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 617-523-3400
CC TELEFAX: 617-523-6440
CC TELEX: 200291
CC INFORMATION FOR SEQ ID NO: 11:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 127 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC MOLECULE TYPE: Peptide
CC TOPOGY: linear
CC HYPOTHETICAL: NO
CC ANTI-SENSE: NO
CC FRAGMENT TYPE: N-terminal
CC ORIGINAL SOURCE:
CC SEQUENCE 127 AA; 14256 MW; 78142 CN;

Query Match 67-74: Score 617; DB 1; Length 127; Best Local Similarity 62.2%; Pred. No. 1.09e-50; Matches 74; Conservative 24; Mismatches 21; Indels 0; Gaps 0;

Db 9 HATKRSLNCDONSNITCCKRDYVDFKDGWWDWIRPEGYQINCMGLCPMHTAGPCTA 68
Qy 1 RARRRPCTCEPATPLCRRDHYDQELGWRDMLQPEGYOLNCGOCPPPHLGSFGIA 60

Db 69 ASPHATVNLKANNIQTAVNSCCVTPARPLSLYLDRANGNVVKTDPDMVYAGC 127
Qy 61 ASFSAVESLILKANNPWPAS-TISCCVTPARPLSLYLDRANGNVVKTDPDMVYAGC 119

RESULT 8 ID US-08-82-577B-2 STANDARD: PRT; 352 AA.

DE Sequence 2, Application US/08482577B
XX Sequence 2, Application US/08482577B
CC Sequence 2, Application US/08482577B
CC Patent No. 5807713
CC GENERAL INFORMATION:
CC APPLICANT: HOTTEN, GERTRUD

INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:

LENGTH: 121 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

IMMEDIATE SOURCE:

CLONE: Inhibin beta A

FEATURE:

NAME/KEY: protein

LOCATION: 1..121

SEQUENCE:

121 AA; 13757 MW; 76294 CN;

Query Match 54.4%; Score 498; DB 3; Length 121;

Best Local Similarity 45.5%; Pred. No. 1.1e-38;

Matches 55; Conservative 32; Mismatches 32; Indels 2; Gaps 2;

Db 1 RRRRGLECDGKVNICCKQFFVFSFKDITGWNWMIAPSGYHANYCEGECPSHIAAGSGSS 60

Qy 1 RARRRPTCEPATPLCCRRDHYDFQELGWRDWLQPEGYQOLNYCSGQCPPHLASPGIA 60

61 LSFHSTVNHYRGRHSFSPANLKSCCPVTKLAPMSMILYDDGQNIKKDIONIVECGC 120

Qy 61 ASFHSAVFS-L-LKANNPWPASTSCCVPTARRPLSLLYDHNNGNNVVKTDVPMWVACGC 118

Db 121 S 121

Qy 119 S 119

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:

LENGTH: 122 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

IMMEDIATE SOURCE:

CLONE: Inhibin-beta-alpha

FEATURE:

NAME/KEY: Protein

LOCATION: 1..122

SEQUENCE:

122 AA; 13894 MW; 77513 CN;

Query Match 54.4%; Score 498; DB 1; Length 122;

Best Local Similarity 45.5%; Pred. No. 1.1e-38;

Matches 55; Conservative 32; Mismatches 32; Indels 2; Gaps 2;

Db 2 RRRRGLECDGKVNICCKQFFVFSFKDITGWNWMIAPSGYHANYCEGECPSHIAAGSGSS 61

Qy 1 RARRRPTCEPATPLCCRRDHYDFQELGWRDWLQPEGYQOLNYCSGQCPPHLASPGIA 60

62 LSFHSTVNHYRGRHSFSPANLKSCCPVTKLAPMSMILYDDGQNIKKDIONIVECGC 121

Qy 61 ASFHSAVFS-L-LKANNPWPASTSCCVPTARRPLSLLYDHNNGNNVVKTDVPMWVACGC 118

Db 122 S 122

Qy 119 S 119

RESULT 15
ID US-08-455-559-23 STANDARD: PRT; 122 AA.

XX
AC
XXXXXX
XX
DT

Sequence 23, Application US/08455559

Sequence 23, Application US/08455559

Patent No. 5801014

GENERAL INFORMATION:

APPLICANT: LEE, SE-JIN

TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:

ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
CITY: LOS ANGELES
STATE: CALIFORNIA
COUNTRY: US

ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,559
FILING DATE: 31-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/003,144
FILING DATE: 12-JAN-1993

ATTORNEY/AGENT INFORMATION:
NAME: WETHERELL, JR., JOHN R.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD2280
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-455-5100
TELEFAX: 619-455-5110

Search completed: Thu Aug 17 10:20:29 2000
Job time : 34 secs.

DR PROSITE: PS00250; "TGF_BETA_1"; 1.
 KW FOLLITROPIN inhibitor; Contraceptive; Hormone; Glycoprotein; Signal.
 FT SIGNAL 1 21
 FT PROPEP 22 236
 FT CHAIN 237 350
 FT DISULFID 240 248
 FT DISULFID 247 315
 FT DISULFID 276 347
 FT DISULFID 280 349
 FT DISULFID 314 319
 FT CARBOHYD 319 350
 FT SEQUENCE 350 AA; 38898 MW; 0C6F6E108E926E3 CRC64;

Query Match 98.9%; Score 906; DB 1; Length 350;
 Best Local Similarity 97.5%; Pred. No. 1. 23e-227; 3; Mismatches 1; Indels 0; Gaps 0;
 Matches 116; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 232 RARRRPTCPETPLCRRRHYPWFQEGWWRDMLQPGYQLYNCSSOCPPHLAGSPGIA 291
 Qy 1 RARRRPTCEPATPLCRRRHYPWFQELGRWDMLQPGYQLYNCSSOCPPHLAGSPGIA 60

292 ASFHSAVFSLLKANNPWPASTSCCVPTARRPLSLYLHDHNGNTWKTDPDMVTEACGCS 350
 Qy 61 ASFHSAVFSLLKANNPWPASTSCCVPTARRPLSLYLHDHNGNTWKTDPDMVTEACGCS 119

RESULT 2
 ID IHBE RAT STANDARD; PRT; 350 AA.
 AC 088959;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DE INHIBIN BETA E CHAIN PRECURSOR (ACTIVIN BETA-E CHAIN).
 GN OS
 OC Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=LIVER, AND LUNG;
 RA O'Bryan M.K., Sebire K., Hedder M.P., Hearn M.T.W., de Kretser D.M.;
 RT "The cloning and regulation of the rat activin beta subunit.";
 RL Submitted (SEP-1998) to the EMBL/Genbank/DBJ databases.
 CC -!- FUNCTION: INHIBINS ARE GONADAL GLYCOPETIDES THAT INHIBIT THE
 SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. ON THE OTHER HAND
 ACTIVINS ACTIVATE THE SECRETION OF FOLLITROPIN. ACTIVINS REGULATE
 GROWTH AND DIFFERENTIATION OF EMBRYONAL CARCINOMA CELLS, INDUCE
 ERYTHROPOEISIS, STIMULATE INSULIN SECRETION, AND PROMOTE NEURAL
 CELL SURVIVAL. ACTIVINS ARE ALSO IMPORTANT IN EMBRYONIC AXIAL
 DEVELOPMENT.
 -!- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS (BY
 SIMILARITY)
 -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

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CC EMBL; AF088925; AAC66741; -
 DR PFAM; PF0019; TGF_Beta; 1.
 DR PRINTS; PRO0438; GFCYSKNOI.
 DR PROSITE: PS00250; TGF_BETA_1; 1.
 KW PROPEP 22 236
 FT CHAIN 237 350
 FT DISULFID 240 248
 FT DISULFID 247 315
 FT DISULFID 276 347
 FT CARBOHYD 319 350
 FT SEQUENCE 350 AA; 38898 MW; 0C6F6E108E926E3 CRC64;

FT DISULFID 280 349
 FT DISULFID 314 350
 FT CARBOHYD 319 350
 FT SEQUENCE 350 AA; 38898 MW; 0C6F6E108E926E3 CRC64;

Query Match 98.1%; Score 899; DB 1; Length 350;
 Best Local Similarity 96.6%; Pred. No. 1. 53e-227; 3; Mismatches 1; Indels 0; Gaps 0;
 Matches 115; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 232 RARRRPTCEPATPLCRRRHYPWFQELGRWDMLQPGYQLYNCSSOCPPHLAGSPGIA 291
 Qy 1 RARRRPTCEPATPLCRRRHYPWFQELGRWDMLQPGYQLYNCSSOCPPHLAGSPGIA 60

292 ASFHSAVFSLLKANNPWPAGSSCCVPTARRPLSLYLDDNGNTWKTDPDMVTEACGCS 350
 Qy 61 ASFHSAVFSLLKANNPWPASTSCCVPTARRPLSLYLHDHNGNTWKTDPDMVTEACGCS 119

RESULT 3
 ID IHBC_MOUSE STANDARD; PRT; 352 AA.
 AC P55104; 061152;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-FEB-2000 (Rel. 39, Last sequence update)
 DE INHIBIN BETA C CHAIN PRECURSOR (ACTIVIN BETA-C CHAIN).
 GN INHBC.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129; TISSUE=LIVER;
 RN MEDLINE; 96435913.
 RA Schmitt J., Hoettner G., Jenkins N.A., Gilbert D.J., Copeland N.G.,
 RA Pohl J., Schiwek H.,
 RT "Structure, chromosomal localization, and expression analysis of the
 mouse inhibin/activin beta C (Inhbc) gene.";
 RL Genomics 32:358-366(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 9623807.
 RA Liu A.-L., Nishimori K., Matzuk M.M.:
 RT "Structural analysis of the mouse activin beta C gene.";
 RL Biochim. Biophys. Acta 1307:145-148(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 CC
 RX MEDLINE; 97224404.
 RA Fang J., Wang S.Q., Smiley E., Bonadio J.,
 RT "Genes coding for mouse activin beta C and activin beta C gene.";
 RT and exhibit a liver-specific expression pattern in adult tissues.";
 RL Biochim. Biophys. Res. Commun. 231:655-661(1997).
 CC
 -!- FUNCTION: INHIBINS ARE GONADAL GLYCOPETIDES THAT INHIBIT THE
 SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. ON THE OTHER HAND
 ACTIVINS ACTIVATE THE SECRETION OF FOLLITROPIN. ACTIVINS REGULATE
 GROWTH AND DIFFERENTIATION OF EMBRYONAL CARCINOMA CELLS, INDUCE
 ERYTHROPOEISIS, STIMULATE INSULIN SECRETION, AND PROMOTE NEURAL
 CELL SURVIVAL. ACTIVINS ARE ALSO IMPORTANT IN EMBRYONIC AXIAL
 DEVELOPMENT.
 -!- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
 CC
 -!- TISSUE SPECIFICITY: MAINLY EXPRESSED IN THE ADULT LIVER.
 CC
 -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 CC

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 CC
 DR EMBL; X90841; CAM62347.1; JOINED.
 DR EMBL; X90842; CAM62347.1; JOINED.
 DR EMBL; X90819; CAM62333.1; -.

EMBL; U40773; AAC52723.1; -
 DR EMBL; U40772; AAC52723.1; JOINED.
 DR EMBL; U95962; AAC53164.1; -
 DR HSSP; P18075; IBMPP.
 DR MGD; MG3:105932; INHBC.
 DR PF00019; TGF-beta; 1.
 DR PRINTS; PR00438; GFCKSKNOT.
 DR PROSITE; PS00250; TGF-BETA.1; 1.
 DR FOLLITROPIN inhibitor; Contraceptive; Hormone; Glycoprotein; Signal.
 DR SIGNAL; 1 18
 FT PROPEP 19 236
 FT PROPEP 237 352
 FT CHAIN 240 352
 FT DISULFID 247 317
 FT DISULFID 276 349
 FT DISULFID 280 351
 FT DISULFID 316 316
 FT CARBOYD 111 111
 FT CARBOYD 143 143
 FT CARBOYD 161 161
 FT CARBOYD 173 173
 FT CARBOYD 243 243
 FT SEQUENCE 352 AA; 39401 MW; 220812FD73717185 CRC64;
 SQ Query Match 69.0%; Score 632; DB 1; Length 352;
 Best Local Similarity 63.6%; Pred. No. 2.46e-148;
 Matches 77; Conservative 26; Mismatches 16; Indels 2; Gaps 2;
 Db 232 RVRGRIGDQGASGCCRCQEEFFVDFREIGWHDNITQPEGYANMFCTGQCPHLAGMGIAS 291
 QY 1 RARRKPTCEPATPLCRRDHVDFQELQWRDNLILQPGYQLNICSQCPHLAGSGAGIA 60
 Db 292 ASFETAVLILKANAAAGTGTGRSSCCYTSRRPLSLYDROSNTIVKTDIDPDMVVAEGCS 351
 QY 61 ASFHSAVFSLKANNPWP-PAS-TSCCVPTARRFLSLLDHNNGNVVKTDVPMVVACGS 118
 Db 352 S 352
 QY 119 S 119

RESULT 4
 ID INHBC-HUMAN STANDARD; PRT; 352 AA.
 AC P55103;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE INHIBIN BETA C CHAIN PRECURSOR (ACTIVIN BETA-C CHAIN).
 GN INHBC
 OS Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 RN [1]
 RN SEQUENCE FROM N.A.
 RP TISSUE-LIVER;
 RX MEDLINE; 95126961.
 RA Hoettgen G., Neidhardt H., Schneider C., Pohl J.;
 RT "Cloning of a new member of the TGF-beta family: a putative new
 activin beta C chain.",
 Biochem. Biophys. Commun. 206:608-613(1995). That inhibit the
 secretion of follitropin by the pituitary gland. On the other hand
 activins activate the secretion of follitropin. Activins regulate
 growth and differentiation of embryonal carcinoma cells, induce
 erythropoiesis, stimulate insulin secretion, and promote neural
 cell survival. Activins are also important in embryonic axial
 development.
 -!- SUBUNIT: Dimeric, linked by one or more disulfide bonds.
 -!- SIMILARITY: Belongs to the TGF-beta family.
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 CC
 DR EMBL; X82540; CA57890.1; -
 DR HSSP; P18075; IBMPP.
 DR MIM; 601233; -
 DR PFAM; PF00019; TGF-beta; 1.
 DR PRINTS; PR00438; GFCKSKNOT.
 DR PROSITE; PS00250; TGF-BETA.1; 1.
 DR SIGNAL; 1 18
 FT PROPEP 19 236
 FT CHAIN 237 352
 FT DISULFID 247 317
 FT DISULFID 276 349
 FT DISULFID 316 316
 FT CARBOYD 110 110
 FT CARBOYD 143 143
 FT CARBOYD 161 161
 FT SEQUENCE 352 AA; 38238 MW; 498476AD82562D3E CRC64;
 SQ Query Match 67.2%; Score 616; DB 1; Length 352;
 Best Local Similarity 63.9%; Pred. No. 1.21e-143;
 Matches 76; Conservative 26; Mismatches 15; Indels 2; Gaps 2;
 Db 234 RRRGIDCOGGSRMCCRCQEEFFVDFREIGWHDNITQPEGYANMFCTGQCPHLAGMGIAS 293
 QY 3 RARRKPTCEPATPLCRRDHVDFQELQWRDNLILQPGYQLNICSQCPHLAGSGAGIA 62
 Db 294 FITAVLILKNTAAAGTGTGRSSCCYTSRRPLSLYDROSNTIVKTDIDPDMVVAEGCS 352
 QY 63 FHSAVFSLKANNPWP-PAS-TSCCVPTARRFLSLLDHNNGNVVKTDVPMVVACGS 119

RESULT 5
 ID INHBC-HORSE STANDARD; PRT; 426 AA.
 AC P55102;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE INHIBIN BETA A CHAIN PRECURSOR (ACTIVIN BETA-A CHAIN).
 GN INHBA
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-OVARY;
 RX MEDLINE; 96031670.
 RA Yoshida S., Yamamotochi K., Hasegawa T., Ikeda A., Suzuki M.,
 RA Chang K., Matsunaga S., Nishihara M., Takahashi M.;
 RT "Molecular cloning of cDNA for equine ovarian inhibin/activin beta A
 subunit.",
 J. Vet. Med. Sci. 57:469-473(1995).
 CC -!- FUNCTION: INHIBIN IS A GONADAL GLYCOPEPTIDE THAT INHIBITS THE
 CC SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. ON THE OTHER HAND
 CC ACTIVIN ACTIVATES THE SECRETION OF FOLLITROPIN. ACTIVIN IS ALSO
 CC -!- SUBUNIT: Dimeric, linked by one or more disulfide bonds.
 CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
 CC INHIBIN B IS A DIMER OF BETA-A AND BETA-B.
 CC ACTIVIN A IS A DIMER OF BETA-A.
 CC ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B.
 CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 CC
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 CC -----
 DR EMBL: X69619; CAA49325.1; -.
 DR PIR: S31440; S31440.
 DR HSSP; P18075; 1BMP.
 DR MGD; MGI:98570; INHBA.
 DR PFAM; PF00019; TGF-beta; 1.
 DR PRAM; PF0688; TGFB_propeptide; 1.
 DR PRINTS; PRO0438; GFCYSKNOT.
 DR PROSITE; PS00250; TGF_BETA_1.
 DR FOLLITROPIN_INHIBITOR; Contraceptive; Hormone; Glycoprotein; Signal.
 FT SIGNAL 1; PROPEP ?
 FT CHAIN 309 424 INHIBIN BETA A CHAIN.
 FT DISULFID 312 320 BY SIMILARITY.
 FT DISULFID 319 389 BY SIMILARITY.
 FT DISULFID 348 421 BY SIMILARITY.
 FT DISULFID 352 423 BY SIMILARITY.
 FT DISULFID 388 388 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 165 165 POTENTIAL.
 SQ SEQUENCE 424 AA; MW: 80251B8754A7213 CRC64;
 Query Match 54.4%; Score 498; DB 1; Length 424;
 Best Local Similarity 45.5%; Pred. No. 2 49e-109; 32; Indels 2; Gaps 2;
 Matches 55; Conservative 32; Mismatches 32;
 DR 304 RRRRGLECDGKVNCKKQFFVSRDIDGNWVIAKPSGHANTEGEGECPHSHTGSS 363
 QY 1 RARRRPCTEPATPLCRRDHVYDQELGRDWILOQEGYOLNQCSGOCPPHLAGSPGIA 60
 Db 364 LSFHSTVINVHMRMRHSFPANLKSCCVPTKLPRMSMLYVDDGQNTIKKDIQNMVVECGC 423
 QY 61 ASPHSAVFS-L-LKANNPWPASTSCCVPTARRPLSLYLHDHGNVVKTDVPMVYEA CGC 118
 Db 424 S 424
 Ov 119 S 119
 DR RESULT 8
 ID INHBA_RAT STANDARD; PRT; 424 AA.
 AC P18331;
 DT 01-NOV-1990 (Rel. 15, Created)
 DT 01-NOV-1990 (Rel. 15, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE INHIBIN BETA A CHAIN PRECURSOR (ACTIVIN BETA-A CHAIN).
 GN INHBA.
 OS Rattus norvegicus (Rat).
 OC Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus
 RN [1] SEQUENCE FROM N.A.
 RX MEDLINE; 91042598.
 RA Woodruff T.K., Meunier H., Jones P.B.C., Hsueh A.J.W., Mayo K.E.;
 RT "Rat inhibin: molecular cloning of alpha- and beta-subunit complementary deoxyribonucleic acids and expression in the ovary.";
 RT Mol. Endocrinol. 1:561-568 (1987).
 DE INHIBIN BETA A CHAIN PRECURSOR (ACTIVIN BETA-A CHAIN).
 GN INHBA.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus
 RN [1] SEQUENCE FROM N.A.
 RP TISSUE=FOLLICULAR FLUID;
 RX MEDLINE; 86092207.
 RA Mason A.J., Hayflick J.S., Ling N., Esch F., Ueno N., Ying S.-Y.,
 RA Guilliman R., Mail H.; Seburg P.H.;
 RT "Complementary DNA sequences of ovarian follicular fluid inhibin show precursor structure and homology with transforming growth factor-beta.";
 RT Nature 318:659-663 (1985).
 RN [2] SEQUENCE OF 309-323.
 RP TISSUE=FOLLICULAR FLUID;
 RX MEDLINE; 92355604.

CC -----
 CC ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B.
 CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 CC -----
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 CC -----
 DR EMBL: M37482; AAC1436.1; -.
 DR PIR; B40056; B40056.
 DR HSSP; P18075; 1BMP.
 DR PFAM; PF00019; TGF-beta; 1.
 DR PRAM; PF0688; TGFB_propeptide; 1.
 DR PRINTS; PRO0438; GFCYSKNOT.
 DR PROSITE; PS00250; TGF_BETA_1.
 DR FOLLITROPIN_INHIBITOR; Contraceptive; Hormone; Glycoprotein; Signal.
 FT SIGNAL 1; PROPEP ?
 FT CHAIN 309 424 INHIBIN BETA A CHAIN.
 FT DISULFID 312 320 BY SIMILARITY.
 FT DISULFID 319 389 BY SIMILARITY.
 FT DISULFID 348 421 BY SIMILARITY.
 FT DISULFID 352 423 BY SIMILARITY.
 FT DISULFID 388 388 BY SIMILARITY.
 FT DISULFID 388 388 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 165 165 POTENTIAL.
 SQ SEQUENCE 424 AA; MW: B2DA7917F50984 CRC54;
 Query Match 54.4%; Score 498; DB 1; Length 424;
 Best Local Similarity 45.5%; Pred. No. 2 49e-109; 32; Indels 2; Gaps 2;
 Matches 55; Conservative 32; Mismatches 32;
 DR 304 RRRRGLECDGKVNCKKQFFVSRDIDGNWVIAKPSGHANTEGEGECPHSHTGSS 363
 QY 1 RARRRPCTEPATPLCRRDHVYDQELGRDWILOQEGYOLNQCSGOCPPHLAGSPGIA 60
 Db 364 LSFHSTVINVHMRMRHSFPANLKSCCVPTKLPRMSMLYVDDGQNTIKKDIQNMVVECGC 423
 QY 61 ASPHSAVFS-L-LKANNPWPASTSCCVPTARRPLSLYLHDHGNVVKTDVPMVYEA CGC 118
 Db 424 S 424
 Ov 119 S 119
 DR RESULT 9
 ID INHBA_PIG STANDARD; PRT; 424 AA.
 AC P03970;
 DT 23-OCT-1986 (Rel. 02, Created)
 DT 23-OCT-1986 (Rel. 02, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE INHIBIN BETA A CHAIN PRECURSOR (ACTIVIN BETA-A CHAIN).
 GN INHBA.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus
 RN [1] SEQUENCE FROM N.A.
 RP TISSUE=FOLLICULAR FLUID;
 RX MEDLINE; 86092207.
 RA Mason A.J., Hayflick J.S., Ling N., Esch F., Ueno N., Ying S.-Y.,
 RA Guilliman R., Mail H.; Seburg P.H.;
 RT "Complementary DNA sequences of ovarian follicular fluid inhibin show precursor structure and homology with transforming growth factor-beta.";
 RT Nature 318:659-663 (1985).
 RN [2] SEQUENCE OF 309-323.
 RP TISSUE=FOLLICULAR FLUID;
 RX MEDLINE; 92355604.

RA Nakamura T., Asashima M., Eto Y., Takio K., Uchiyama H., Moriya N.,
 RA Ariizumi T., Yashiro T., Sugino K., Titani K., Sugino H.;
 RT "Isolation and characterization of native activin B";
 RL J. Biol. Chem. 267:1685-16389(1992);
 CC .-!- FUNCTION: INHIBIN IS A GONADAL GLYCOPEPTIDE THAT INHIBITS THE
 SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. ON THE OTHER HAND
 ACTIVIN ACTIVATES THE SECRETION OF FOLLITROPIN. ACTIVIN IS ALSO
 IMPORTANT IN EMBRYONIC AXIAL DEVELOPMENT.
 CC .-!- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
 CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
 CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
 CC ACTIVIN A IS A DIMER OF BETA-A AND BETA-B.
 CC .-!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 CC
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 or send an email to license@isb-sib.ch).
 CC
 DR EMBL: X03266; CAZ27020.1; -.
 DR HSSP: P18075; IBMP.
 DR PFAM: PF00019; TGF-beta; 1.
 DR PFM: PF0688; TGFb_propeptide; 1.
 DR PRINTS: PRO0438; GFCYSNOT.
 DR PRINTS: PRO0070; INHIBINB.
 DR PROTE: PS00250; TGF_BETA_1; 1.
 DR KW Follitropin inhibitor; Contraceptive; Hormone; Glycoprotein; Signal.
 FT SIGNAL 1
 FT PROPEP ? 308
 FT CHAIN 309 424
 FT DISULFID 312 320
 FT DISULFID 319 389
 FT DISULFID 348 421
 FT DISULFID 352 423
 FT DISULFID 388 389
 FT CARBOHYD 4165 165
 SQ SEQUENCE 424 AA; 47476 MW; 436BC62226EDAF52 CRC64;
 DR
 DR Query Match 54.4%; Score 498; DB 1; Length 424;
 DR Best Local Similarity 45.5%; Pred. No. 2.49e-109;
 DR Matches 55; Conservative 32; Mismatches 32; Indels 2; Gaps 2;
 DR PRINTS: PRO0438; GFCYSNOT.
 DR PROTE: PS00250; TGF_BETA_1; 1.
 DR PRINTS: PRO0070; INHIBINB.
 DR PROTE: PS00250; TGF_BETA_1; 1.
 DR KW Follitropin inhibitor; Contraceptive; Hormone; Glycoprotein;
 DR Signal. 1
 DR PROPEP 29 309
 DR CHAIN 310 425
 DR DISULFID 313 321
 DR DISULFID 320 390
 DR DISULFID 349 422
 DR DISULFID 353 424
 DR DISULFID 389 389
 DR CARBOHYD 4165 165
 SQ SEQUENCE 425 AA; 47521 MW; 2D879D7197CDA37 CRC64;
 DR
 DR Query Match 54.4%; Score 498; DB 1; Length 425;
 DR Best Local Similarity 45.5%; Pred. No. 2.49e-109;
 DR Matches 55; Conservative 32; Mismatches 32; Indels 2; Gaps 2;
 DR PRINTS: PRO0438; GFCYSNOT.
 DR PROTE: PS00250; TGF_BETA_1; 1.
 DR PRINTS: PRO0070; INHIBIN_B_CHAIN_PRECURSOR (ACTIVIN_BETA_A_CHAIN).
 DR
 DR 305 RRRRGLEDGKKNICRKOFFVSKFDIGWANDMILAPSQHANYCEGCGCPSPHIAGTGS 364
 DR .-!- 1 RARRRPTCEPATPLCCRRDHVYDFQELGWRWNIQPGYQOLNYC5GQCPPLAGSPGIA 60
 DR
 DR 364 LSHSTVNHRYRGHSPFANLKSCCVPTKLKPMMSLYDDQGONIKKDIQMIIVECGC 423
 DR .-!- 51 ASRHSAVS-L-IKANNPWAStSCCPVTPARRPLSLIYLDHNGNVKTDVPMVEAGC 118
 DR
 DR 424 S 424
 DR PRINTS: PRO0438; GFCYSNOT.
 DR PROTE: PS00250; TGF_BETA_1; 1.
 DR PRINTS: PRO0070; INHIBINB.
 DR PROTE: PS00250; TGF_BETA_1; 1.
 DR KW Follitropin inhibitor; Contraceptive; Hormone; Glycoprotein;
 DR Signal. 1
 DR PROPEP 28 309
 DR CHAIN 310 425
 DR DISULFID 313 321
 DR DISULFID 320 390
 DR DISULFID 349 422
 DR DISULFID 353 424
 DR DISULFID 389 389
 DR CARBOHYD 4165 165
 SQ SEQUENCE 425 AA; 47521 MW; 2D879D7197CDA37 CRC64;
 DR
 DR Query Match 54.4%; Score 498; DB 1; Length 425;
 DR Best Local Similarity 45.5%; Pred. No. 2.49e-109;
 DR Matches 55; Conservative 32; Mismatches 32; Indels 2; Gaps 2;
 DR PRINTS: PRO0438; GFCYSNOT.
 DR PROTE: PS00250; TGF_BETA_1; 1.
 DR PRINTS: PRO0070; INHIBIN_B_CHAIN_PRECURSOR (ACTIVIN_BETA_A_CHAIN).
 DR
 DR 365 LSHSTVNHRYRGHSPFANLKSCCVPTKLKPMMSLYDDQGONIKKDIQMIIVECGC 424
 DR .-!- 61 ASRHSAVS-L-IKANNPWAStSCCPVTPARRPLSLIYLDHNGNVKTDVPMVEAGC 118
 DR
 DR {1} .-!
 DR .-!

Db 425 S 425
Qy 119 S 119

RESULT 11
ID IHBA_HUMAN STANDARD; PRT; 426 AA.
AC P08476; Q14599; P08476; Q14599; 08, Created
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE INHIBIN BETA A CHAIN PRECURSOR (ACTIVIN BETA-A CHAIN) (ERYTHROID DIFFERENTIATION PROTEIN) (EDF).
GN INHBA.
OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Homo sapiens (Human).
[1] SEQUENCE FROM N.A.
MEDLINE; 8618683.
RA Mason A.J., Niall H.D., Seeburg P.H.;
RT "Structure of two human ovarian inhibins";
RL Biochem. Biophys. Res. Commun. 135:957-964(1986).
RN [2] SEQUENCE FROM N.A.
MEDLINE; 88190086.
RA Murata M., Eto Y., Shibai H., Sakai M., Muramatsu M.; Muramatsu M.;
RT of the inhibin beta A chain";
RL PRO. NATL. ACAD. SCI. U.S.A. 85:2434-2438(1988).
RN [3] SEQUENCE FROM N.A.
MEDLINE; 92135888.
RA Tanimoto K., Handa S.I., Ueno N., Murakami K., Fukamizu A.;
RT "Structure and sequence analysis of the human activin beta A subunit gene";
RL DNA Seq. 2:103-110(1991).
RN [4] SEQUENCE OF 311-426 FROM N.A.
RP MEDLINE; 87005283.
RX
RA Stewart A.G., Milborrow H.M., Ring J.M., Crowther C.E., Forage R.G.;
RT Human inhibin genes: Genomic characterisation and sequencing";
RL FEBS Lett. 206:329-334(1986).
RN [5] SEQUENCE OF 311-426 FROM N.A.
RP TISSUE-TESTS;
RA
CC Submitted (MAY-1993) to the EMBL/GenBank/DBJ databases.
- FUNCTION: INHIBIN IS A GONADAL GLYCOPEPTIDE THAT INHIBITS THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. ON THE OTHER HAND ACTIVIN ACTIVATES THE SECRETION OF FOLLITROPIN. ACTIVIN IS ALSO IMPORTANT IN EMBRYONIC AXIAL DEVELOPMENT.
CC - SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
CC INHIBIN IS A DIMER OF ALPHABETAB.
CC INHIBIN B IS A DIMER OF ALPHABETAB.
CC ACTIVIN A IS A DIMER OF BETA-A.
CC ACTIVIN B IS A DIMER OF BETA-A AND BETA-B.
CC - SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC
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RESULT 12
ID IHBA_CHICK STANDARD; PRT; 424 AA.
AC P27092; Q90697; P27092; Q90697; 08, Created
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DE INHIBIN BETA A CHAIN PRECURSOR (ACTIVIN BETA-A CHAIN).
GN INHBA.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Gallus gallus; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN [1] SEQUENCE FROM N.A.
RP STRAIN=WHITE LEGHORN;
RA Huang J.X.;
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
RN [2] SEQUENCE FROM N.A.
RP STRAIN=WHITE LEGHORN;
RA MEDLINE; 96380183.
RN [3] SEQUENCE OF 317-349 FROM N.A.
RP TISSUE=HYPOBLAST;
RX MEDLINE; 91029482.

DR EMBL; A14422; CAA01159.1; -.
DR EMBL; X72498; CAA51163.1; -.
DR PIR; A30884; A30884.
DR PIR; B24248; B24248.
DR PIR; B23556; B23556.
DR PIR; S30488; S30488.
DR HSSP; RP18075; 1BMP.
DR MIM; 147290; -.
DR PROSITE; PS00250; TGF-BETA_1.
DR PFAM; PPF00019; TGF-BETA_propeptide.
DR PRINTS; PRO0438; GFCYSNOT.
DR PRIMIS; PR00570; INHIBINBA.
DR PROSITE; PS00250; TGF-BETA_1.
DR KW Follitropin inhibitor; Contraceptive; Hormone; Glycoprotein; Signal.
FT SIGNAL 1 28
FT PROPEP 29 310
FT CHAIN 311 425
FT DISULFID 314 322
FT DISULFID 321 391
FT DISULFID 350 423
FT DISULFID 354 425
FT DISULFID 390 390
FT CARBOHYD 165 165
FT CONFLICT 379 379
FT SEQUENCE 426 AA: 47442 MW: 201CDDBF99CB6919 CRC64;
Query Match 54.4%; Score 498; DB 1; Length 426;
Best Local Similarity 45.4%; Pred. No. 2; 4.9e-109;
Matches 55; Conservative 32; Mismatches 32; Indels 2; Gaps 2;
Db 306 RRRRGLECDGKVNICCKQFFVSKFDGWNNTIAPSGVHANYCCEGCPSPHAGTSGSS 365
Qy 1 RARRRTPTCEPATPLCCRRDHYDQEGLGWRWNIQPEGYQOLNICSQCQCPHLAGSPGIA 60
Db 365 LSFHSTVNHYRGRHSFANKSKSCCPYTKLPPMSMLYYDQGQNTIKKDDQNNIVBECGC 425
Qy 61 ASFHSAVFS-L-LKANNPPASTSCCVPTARRPLSLYLDHNGNVVTDVPMVVERACGC 118
Db 426 S 426
Qy 119 S 119

DR EMBL; X04477; CAA28041.1; -.
DR EMBL; X57578; CAA40805.1; -.
DR EMBL; X57579; CAA40805.1; JOINED.
DR EMBL; X57579; CAA40805.1; -.
DR EMBL; J03634; AAA35787.1; -.

QY	1 RARRRTPTCERATPLCCRRDHVYDQELGRDWLILQPEGYQLNYCSGQCPPLAGSPGIA 60	Query Match	51.4%	Score 471;	DB 1;	Length 255;
Db	332 SSFHTRAVNQYRMGLNPGLPNTVNCCPTKUSTMNLVYDFDDEYNTVKRDVNPMLVECCCA 391	Best Local Similarity	48.3%	Pred. No. 1	4.5e-101;	
QY	61 ASFHSAVFSLLKANNPWPAST-SCCPTTARPLSLYLDRHNGNVKTDVPMVACGCS 119	Matches	58;	Conservative	27;	Mismatches 34;
RESULT	14	Indels	1;	Gaps	1;	
ID	IHB-B MOUSE STANDARD; PRT; 255 AA.					
AC	004939; 001277;					
DT	01-FEB-1994 (Rel. 28, Created)					
DT	01-NOV-1997 (Rel. 35, Last sequence update)					
DT	01-NOV-1997 (Rel. 35, Last annotation update)					
DE	INHIBIN BETA B CHAIN PRECURSOR (ACTIVIN BETA-B CHAIN) (FRAGMENT).					
GN	INHBB.					
OS	MUS musculus (Mouse).					
OC	Eukaryota; Metazoa; Chordata; Craniata; vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.					
RA	[1] SEQUENCE OF 1-234 FROM N.A.					
RC	STRAIN=CBA X NMR1; TISSUE=TESTIS;					
RX	MEDLINE: 95344997.					
RA	Ritvos O., Tuuri T., Eramaa M., Sainio K., Hilden K., Saxen L., Gilbert S.;					
RT	"Activin disrupts epithelial branching morphogenesis in developing glandular organs of the mouse.";					
RL	Mech. Dev., 50:229-245(1995).					
RN	[2]					
RP	SEQUENCE OF 134-255 FROM N.A.					
RX	Albano P.M., Groome N., Smith J.C.;					
RA	"Activins are expressed in preimplantation mouse embryos and in ES and EC cells and are regulated on their differentiation.";					
RT	Development 117:711-723(1993).					
CC	-!- FUNCTION: INHIBIN IS A GONADAL GLYCOPETIDE THAT INHIBITS THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. ON THE OTHER HAND ACTIVIN ACTIVATES THE SECRETION OF FOLLITROPIN. ACTIVIN IS ALSO IMPORTANT IN EMBRYONIC AXIAL DEVELOPMENT.					
CC	-!- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.					
CC	INHIBIN A IS A DIMER OF ALPHA AND BETA-A.					
CC	INHIBIN B IS A DIMER OF ALPHA AND BETA-B.					
CC	ACTIVIN A IS A DIMER OF BETA-A.					
CC	ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B.					
CC	-!- TISSUE SPECIFICITY: UTERUS, TESTIS, OVARY, LUNG, KIDNEY, BRAIN, CJ7 EMBRYONIC STEM CELLS, AND POSSIBLY IN LIVER.					
CC	-!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.					
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CC	PROSITE: PS00019; TGF-beta; 1.					
DR	EMBL: X83376; CAA58290; 1. Folliotropin inhibitor; Contraceptive; Hormone; Glycoprotein.					
FT	NON_TER 1					
PROPEP	<1 140 POTENTIAL.					
FT	CHAIN 141 255 INHIBIN BETA B CHAIN.					
FT	DISULFID 144 152 BY SIMILARITY.					
FT	DISULFID 151 220 BY SIMILARITY.					
FT	DISULFID 180 252 BY SIMILARITY.					
FT	DISULFID 184 254 BY SIMILARITY.					
FT	DISULFID 219 219 INTERCHAIN BY SIMILARITY.					
FT	CONFLICT 135 135 H -> D (IN REF. 2).					
SEQUENCE	255 AA: 229178 MW: 2524B21DC648D9A9 CRC64;					
DR	X03367; CAA27021; 1. Folliotropin inhibitor; Contraceptive; Hormone; Glycoprotein.					
DR	PROTEIN: A01394; WPGCB.					
DR	HSSP; P18075; IBM.					
DR	PFAM: PF00019; TGF-beta; 1.					
DR	DR PROSITE: PS000250; TGF_BETA_1; 1.					
DR	KW Folliotropin inhibitor; Contraceptive; Hormone; Glycoprotein.					
FT	NON_TER 1					
PROPEP	<1 234					
FT	CHAIN 235 349 INHIBIN BETA B CHAIN.					
FT	DISULFID 238 246 BY SIMILARITY.					
FT	DISULFID 245 314 BY SIMILARITY.					

Search completed: Thu Aug 17 10:17:28 2000
Runtime : 30 secs.

100

AC 098861; DT 01-FEB-1997 (TREMBREL_02, Created)
 DT 01-NOV-1999 (TREMBREL_12, Last annotation update)
 DE ACTIVIN BETA-B SUBUNIT (FRAGMENT).
 OS Cynops pyrrhogaster (Japanese common newt).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
 OC Batrachia; Caudata; Salamandroidea; Salamandridae; Cynops.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BLOOD;
 RX MEDLINE: 96295508
 RA YAMAMOTO T., NAKAYAMA Y., ABE S.;
 RT "Expression of activin beta subunit genes in Sertoli cells of newt
 testes.";
 RT Biochem. Res. Commun. 224:451-456(1996).
 CC -1- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.
 DR EMBL: D84517; BAA12694.1; -.
 DR HSSP; P18075; IBM.P.
 DR PROSITE; PS00250; TGF-BETA; 1.
 DR PFAM; PF00019; TGF-beta; 1.
 DR GLICOPROTEIN; 1
 FT NON-TER 102 102 AA; 11849 MW; 4B6A0E7C CRC32;
 SQ SEQUENCE 102 AA; 11849 MW; 4B6A0E7C CRC32;
 Query Match 43.3%; Score 397; DB 13; Length 102;
 Best Local Similarity 50.0%; Pred. No. 1.0(e-71);
 Matches 51; Conservative 21; Mismatches 29; Indels 1; Gaps 1;
 DR 3 TNLCCRCQOFYIDFLIGNDWILAPAGYFGNYCEGSPAYLAGVPGSASSEHTAVNQYR 62
 QY 13 TPLCCRRDHYVDFQELGRWDWILQPEGYQOLNYCQGQCPPLAGSPGIRASFHSAFSLIK 72
 DB 63 MRLQIPLGVNSCCICPTKISTMSMLYFDDDEYNTVKRDVNMIV 104
 QY 73 ANNPPWPAST-SCCVPTARRPLSLYLDHNGNVTKVTDVDMV 113
 RESULT 10
 ID Q90390 PRELIMINARY; PRT; 102 AA.
 AC Q90390;
 RT 01-NOV-1996 (TREMBREL_01, Created)
 DT 01-NOV-1996 (TREMBREL_01, Last sequence update)
 DE ACTIVIN BETA-A SUBUNIT (FRAGMENT).
 OS Carassius auratus (Goldfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
 OC Neopterygii; Teleostei; Euteleostei; Ostrariophysi; Cypriniformes;
 OC Cyprinidae; Cyprinidae; Cyprininae; Carassius.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BLOOD;
 RX MEDLINE: 93390666.
 RA GE W., GALLIN W.J., STROBECK C., PETER R.E.;
 RT "Cloning and sequencing of goldfish activin subunit genes: strong
 structural conservation during vertebrate evolution.";
 RT Biochem. Biophys. Res. Commun. 193:711-717(1993).
 CC -1- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.
 DR EMBL: L15339; AAA9162.1; -.
 DR HSSP; P18075; IBM.P.
 DR PROSITE; PS00250; TGF-BETA; 1.
 DR PFAM; PF00019; TGF-beta; 1.
 DR GLYCOPROTEIN.
 FT NON-TER 102 102 AA; 11342 MW; 89F12412 CRC32;
 SQ SEQUENCE 102 AA; 11342 MW; 89F12412 CRC32;
 Query Match 42.1%; Score 386; DB 13; Length 102;
 Best Local Similarity 51.0%; Pred. No. 6.1(e-69);
 Matches 50; Conservative 19; Mismatches 28; Indels 1; Gaps 1;
 DR 5 LCCRCQYIDFLIGNDWILAPAGYFGNYCEGSPAYLAGVPGSASSEHTAVNQYR 64
 QY 15 LCCRCRDHYVDFQELGRWDWILQPEGYQOLNYCQGQCPPLAGSPGIRASFHSAFSLIKAN 74
 DB 65 GHSPGSVNSCCICPTKISTMSMLYFDDDEYNTVKRDVNMIV 102
 QY 75 NHPPAST-SCCVPTARRPLSLYLDHNGNVTKVTDVDM 111
 RESULT 12
 ID Q90388 PRELIMINARY; PRT; 102 AA.
 AC Q90388;
 RT 01-NOV-1996 (TREMBREL_01, Created)
 DT 01-NOV-1996 (TREMBREL_01, Last sequence update)
 DE ACTIVIN BETA-B-1 SUBUNIT (FRAGMENT).
 OS Carassius auratus (Goldfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
 OC Neopterygii; Teleostei; Euteleostei; Ostrariophysi; Cypriniformes;
 OC Cyprinidae; Cyprinidae; Cyprininae; Carassius.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BLOOD;
 RX MEDLINE: 93390666.
 RA GE W., GALLIN W.J., STROBECK C., PETER R.E.;
 RT "Cloning and sequencing of goldfish activin subunit genes: strong
 structural conservation during vertebrate evolution.";
 RT Biochem. Biophys. Res. Commun. 193:711-717(1993).
 CC -1- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.
 DR EMBL: L15340; AAA9160.1; -.
 DR HSSP; P10600; ITCR.
 DR PROSITE; PS00250; TGF-BETA; 1.
 DR PFAM; PF00019; TGF-beta; 1.
 DR GLYCOPROTEIN.
 FT NON-TER 102 102 AA; 11849 MW; 4B6A0E7C CRC32;
 SQ SEQUENCE 102 AA; 11849 MW; 4B6A0E7C CRC32;
 Query Match 42.2%; Score 387; DB 13; Length 102;
 Best Local Similarity 43.4%; Pred. No. 3.4(e-69);
 Matches 43; Conservative 29; Mismatches 25; Indels 2; Gaps 2;
 DR 4 VCKKRQFYVNFKDIGWSDWMIAPSGYHANYCEGDCPSHVASTGSAFSFHSTVINYRMR 63

